

Linking habitat heterogeneity to genetic partitioning in the rocky subtidal using black surfperch (*Embiotoca jacksoni*)



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Introduction

Habitat complexity and composition can play an important role in structuring populations of marine organisms (Pittman et al. 2010). Here we explore the role of habitat complexity (three dimensional habitat structure) and habitat composition (abundance and distribution of habitat types) in structuring genetic variation in populations of black surfperch *Embiotoca jacksoni*, within Monterey Bay, California.



Recent landscape based ecological studies in nearshore marine systems have demonstrated how landscape metrics (eg. habitat complexity) can affect the location of species boundaries (Robles et al. 2010), and affect species movement and patterns of distribution (Zajac 2008). These studies provide a framework for assessing how landscape variables drive the persistence and composition of marine populations. Variables such as physical and biological habitat can be heterogeneous and spatially variable in composition driving population structuring in low mobility species.

Methods

For this study we used SCUBA to collect biological samples from six research sites around the Monterey peninsula (figure 1). Using These samples, seafloor mapping data, and allele frequencies quantified using 10 microsatellite markers we will use generalized linear models to examine the relation ship between variables (figure 2).

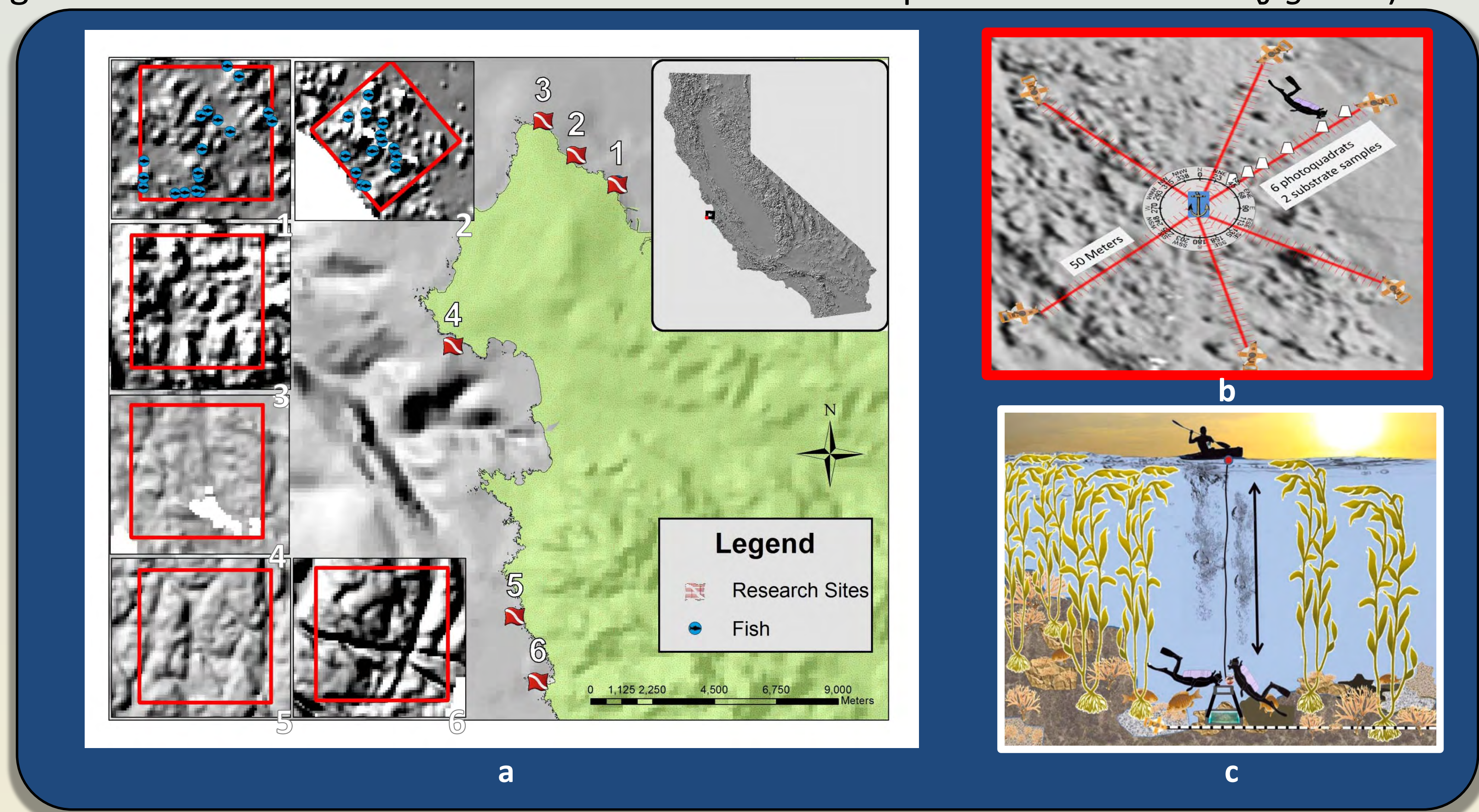


Figure 1. Field protocols for sample collection a) Six 100 X 100 meter research sites along Monterey peninsula with shaded bathymetry background. Similar in depth and rocky reef habitat b) Using SCUBA site sampling procedure with 16, 50 meter transects swam on random headings collecting six random photoquadrats and two random substrate samples. We opportunistically collected 20 black perch at each site using a pole spear. c) Photoquadrat, substrate samples, and fish collection georeferenced points were collected by kayak with a handheld GPS to record locations from a marker float deployed by divers.

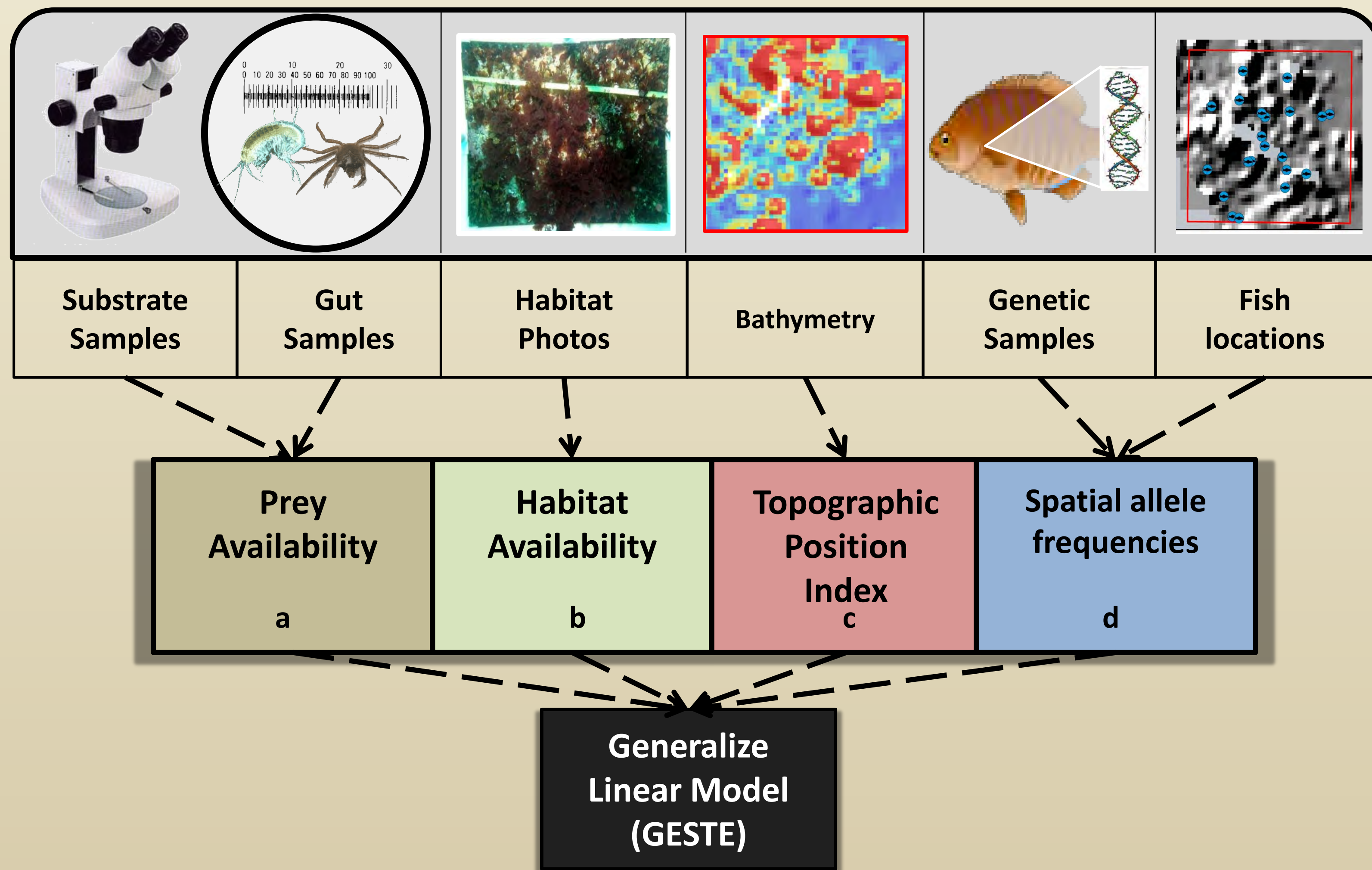


Figure 2 . Schematic of model inputs .a) We counted and quantified biomass of small invertebrates from stomach samples of all fish and substrate samples to calculate prey availability. **b)** Habitat availability was calculated using photoquadrats to quantify percent cover of habitat types. These data were interpolated using ArcMap to create habitat rasters. **c)** Using ArcMap, two meter resolution bathymetry data was used to calculate topographic position index. **d)** Tissue samples from each individual surfperch will be used to establish allele frequency data using 10 microsatellite markers. We will use GESTE (Foll and Gaggiotti 2006), a statistical program that introduces non genetic data via prior distributions of population specific *Fst*'s modeled using generalized linear models. GIS will be used to visualize and analyze the relationship between subtidal landscape variables and genetic diversity in black surfperch populations.

Nearshore rocky reefs along the California coast provide a topographically complex habitat characterized by canopy forming and benthic macroalgae that are a major source of habitat. This habitat provides adult and newly recruited fish with structural refugia, feeding locations, and food derived from secondary productivity. Black surfperch are a common species in rocky reef habitat. Black surfperch have no pelagic larval stage, limited adult dispersal, and associate strongly with benthic habitat making them an excellent model system for this study.



We are using a landscape genetic approach to model how landscape metrics (prey availability, habitat availability, and physical characterization) influence allele frequencies of surfperch and at which scales this relationship becomes ecologically significant via structuring of the population. **This study will provide methods to determine the scales at which genetic diversity becomes ecologically significant and will provide marine managers with methods to estimate the impact of proposed management actions** that may fragment critical subtidal habitats and affect the maintenance of genetic diversity in nearshore populations of marine organisms.

Preliminary Results

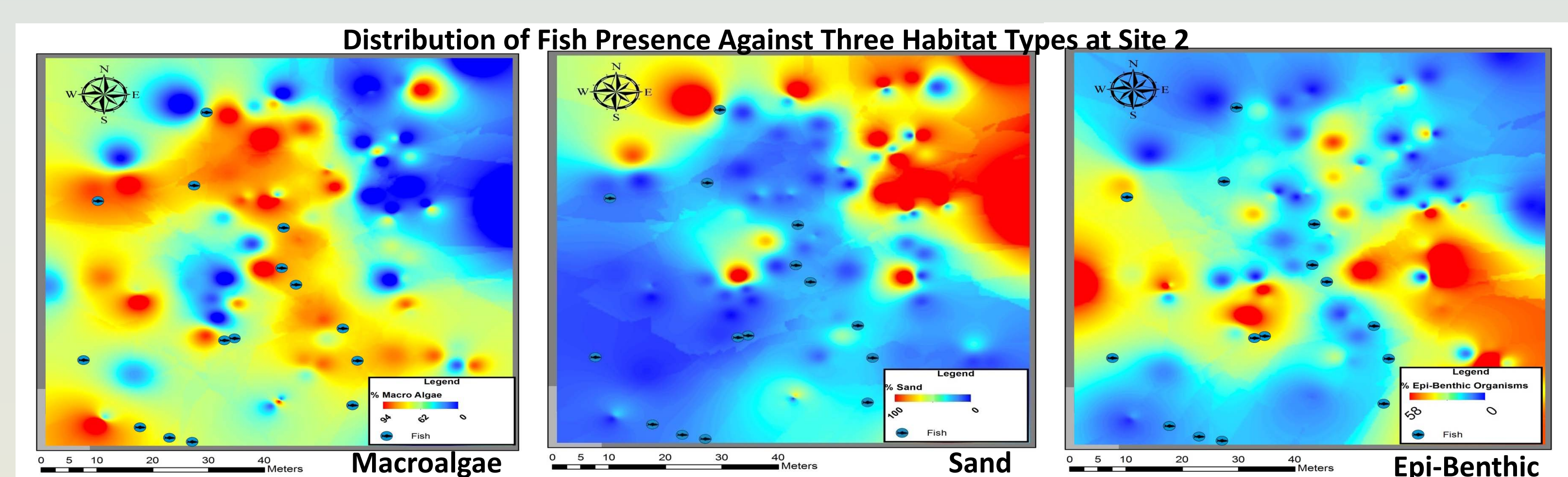


Figure 3. Raster maps of black surfperch distribution at site 2 showing a positive relationship with the macroalgae habitat group, a negative relationship with sandy habitat, and a negative relationship with low structure epi-benthic organisms. Though none of the relationships were significant across the two sites sampled to date.

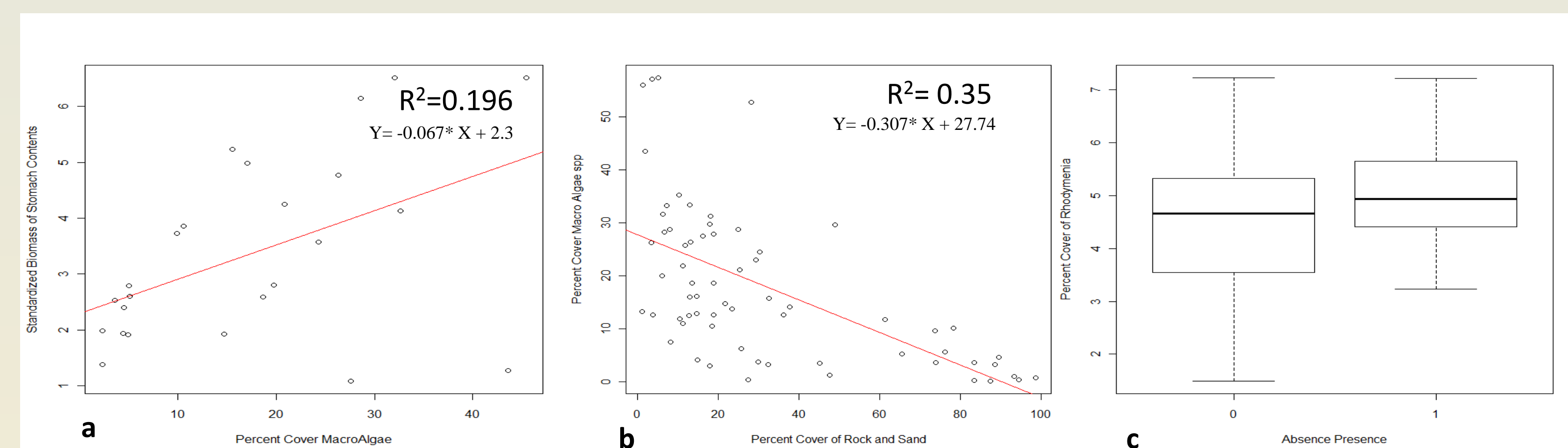


Figure 4. Regression graphs showing a) significant ($p= <0.05$) positive relationship between biomass of prey for surfperch, standardized for fish body size and percent cover of macroalgae habitat. b) The significant negative relationship between macroalgae and sandy habitat. c) Boxplot of difference between presence and absence data as a function of percent cover of Rhodymenia habitat type, a sub-group of the macroalgae group.

Discussion

These preliminary results suggest patterns of fish association with specific habitat groups. The surfperch showed an aversion to open sand habitats across sites while associating with macroalgae habitats. There was a significant relationship between standardized biomass of prey items consumed and percent cover of macroalgae. There was a significant negative relationship between the macro algae and the sandy habitat suggesting an interaction between the biological and physical variables. This also suggests that the surfperch are associating with specific habitat types tied to resource availability. This spatial structuring may lead to genetic partitioning within subpopulations of black surfperch.

Future efforts include completion of sampling for all sites and adding environmental prey availability and the genetic data. We will calculate the allele frequencies within and among sites using microsatellite markers. Finally we will run and evaluate our model for its predictive ability. This will help provide a spatially structured framework for integrating genetic information to an ecosystem management approach.

Citations

Foll M, Gaggiotti O. 2006. Identifying the environmental factors that determine the genetic structure of populations. *Genetics* 174(2):875-891.
Pittman SJ, McAlpine C, Pittman K. 2010. Linking fish and prawns to their environment: A hierarchical landscape approach. *Marine Ecology Progress Series* 283:233-254.
Robles CD, Garza C, Desharnais Ra, Donahue MJ. 2010. Landscape patterns in boundary intensity: A case study of mussel beds. *Landscape Ecology* 25(5):745-759.
Zajac RN. 2008. Challenges in marine, soft-sediment benthoscape ecology. *Landscape Ecology* 23:7-18.

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